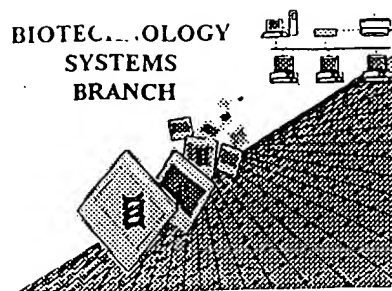


## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/762,021  
Source: PCT09  
Date Processed by STIC: 7/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED      SUGGESTED CORRECTION

SERIAL NUMBER: 09/762,021

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos      was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will  
     prevent "wrapping."
  
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering      use space characters, instead.
  
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
     ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**  
     each n or Xaa can only represent a single residue. Please present the maximum number of each  
     residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"      sequences(s)     . Normally, PatentIn would automatically generate this section from the  
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
     the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
     Artificial or Unknown sequences.
  
- 7      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     This sequence is intentionally skipped  
  
     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)      <210> sequence id number  
     <400> sequence id number  
     000
  
- 9      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)      Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response      scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
     is Artificial Sequence
  
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
     "Unknown." Please explain source of genetic material in <220> to <223> section.  
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PCT

## RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/762,021

TIME: 15:50:32

Input Set : A:\Dex-0039.app

Output Set: N:\CRF3\07032001\I762021.raw

W--> 2 <130> FILE REFERENCE: DEX-0039  
 W--> 0 <110> APPLICANT: DEX-0039  
 W--> 0 <120> TITLE INVENTION:  
 C--> 4 <140> CURRENT APPLICATION NUMBER: US/09/762,021  
 C--> 5 <141> CURRENT FILING DATE: 2001-06-11

Does Not Comply  
 Corrected Note Needed

7 <150> PRIOR APPLICATION NUMBER: 60/095,231  
 8 <151> PRIOR FILING DATE: 1998-08-04

10 <160> NUMBER OF SEQ ID NOS: 3  
 12 <170> SOFTWARE: PatentIn Ver. 2.0

14 &lt;210&gt; SEQ ID NO: 1

15 &lt;211&gt; LENGTH: 1710

16 &lt;212&gt; TYPE: DNA

17 &lt;213&gt; ORGANISM: Homo sapiens

19 &lt;220&gt; FEATURE:

20 &lt;221&gt; NAME/KEY: unsure

21 &lt;222&gt; LOCATION: (1704)

23 &lt;400&gt; SEQUENCE: 1

24 ggcagagcga ctgaagacca gcctgcagaa ggctctggag gaagagctgg agcaaagacc 60  
 25 tcgacttggg ggccttcagc caggccagga cagatggagg gggcctgcta tggaaaggcc 120  
 26 gctccctatg gagcaggcac gctatctgga gccggggatc cctccagaac agccccacca 180  
 27 gaggacccta gagcacagcc tcccaccatc cccaaggccc ctgccacgcc acaccagtgc 240  
 28 ccgagaacca agtgccttta ctctgcctcc tccaaggcgg tcctcttccc ccgaggaccc 300  
 29 agagagggag gaggaagtgc tgaaccatgt cctaaggggac attgagctgt tcatgggaaa 360  
 30 gctgggagaag gccacggcaa agaccagcag gaagaagaaa tttgggaaaa aaaacaagga 420  
 31 ccaggggagg ctacccagg cacagtacat tgactgcttc cagaagatca agtacagctt 480  
 32 caacctcctg ggaaggctgg ccacctggct gaaggagaca agtgcccctg agctcgtaca 540  
 33 catcctcttc aagtcctga acttcactct ggccagggtc cctgaggctg gcctagcagc 600  
 34 ccaagtgate tcacctctcc tcacctctaa agctatcaac ctgctacagt cctgtctaag 660  
 35 cccacctgag agtaaccttt ggatgggggtt gggcccagcc tggaccacta gccggggcga 720  
 36 ctggacaggc gatgagcccc tgccctacca acccacattc tcagatgact ggcaacttcc 780  
 37 agagccctcc agccaagcac ccttaggata ccaggaccct gtttcccttc ggcgggggaa 840  
 38 tcataggtta gggagcacct cacactttcc tcaggagaag acacacaacc atgaccctca 900  
 39 gcctggggac cccaactcca ggccctccag ccccaaacct gccagccag ccctgaaaat 960  
 40 gcaagtcttg tacgagtttg aagctaggaa cccacgggaa ctgactgttg tccagggaga 1020  
 41 gaagctggag gttctggacc acagcaagcg gtggtggctg gtgaagaatg agcggggacg 1080  
 42 gagcggtac attccaagca acatcctgga gcccctacag ccggggaccc ctgggaccca 1140  
 43 gggccagtca ccctctcggg ttccaatgct tcgacttagc tcgaggcctg aagaggtcac 1200  
 44 agactggctg caggcagaga acttctccac tgccacggtg aggacacttg ggtccctgac 1260  
 45 ggggagccag ctacttcgca taagacctgg ggagctacag atgctatgtc cacaggaggc 1320  
 46 cccacgaatc ctgtcccggc tggaggctgt cagaaggatg ctggggataa gcccttaggc 1380  
 47 accagcttag acacctccaa gaaccaggcc ccgctgatgc aagatggcag atctgatacc 1440  
 48 cattagacc ccgagaattc ctctctgga tcccagtttg cagcaaaacc cacacccag 1500  
 49 ctcacacagc aaaaacaatg gacaggccca gaggtgaag caaacagtgt cccttctggc 1560  
 50 tgtgttggag cctccccagt aaccacctat ttattttacc tctttcccaa acctggagca 1620  
 51 tttatgccta ggcttgtcaa gaatctgttc agtccctctc cttctcaata aaagcatctt 1680  
 W--> 52 caagcttgta aaaaaaaaaa taagataaa 1710  
 54 <210> SEQ ID NO: 2

See item #9 on Error Summary  
 SHEET

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/762,021

DATE: 07/05/2001

TIME: 15:50:32

Input Set : A:\Dex-0039.app

Output Set: N:\CRF3\07032001\I762021.raw

55 &lt;211&gt; LENGTH: 1109

56 &lt;212&gt; TYPE: DNA

57 &lt;213&gt; ORGANISM: Homo sapiens

59 &lt;400&gt; SEQUENCE: 2

```

60 gggaaccacc ttctgtagga cagtcaccag gccagatcca gaagcctctc taggctccag 60
61 ctttctctgt ggaagatgac agcaattata gcaggaccct gccaggctgt cgaaaagatt 120
62 ccgcaataaa actttgccag tgggaagtac ctagtgaaac ggcctaagat gccacttctt 180
63 ctcatgtccc aggcttgagg ccctgtggtc cccatccttg ggagaagtca gctccagcac 240
64 catgaagggc atcctcggtt ctggtatcac tgcagtgtt gttgcagctg tagaatctct 300
65 gagctgcgtg cagtgttaatt catgggaaaa atcctgtgtc aacagcattg cctctgaatg 360
66 tccctcacat gccaacacca gctgtatcag ctctcagcc agctcctctc tagagacacc 420
67 agtcagatta taccagaata tgttctgtct agcggagaac tgcagtgagg agacacacat 480
68 tacagccttc actgtccacg tgtctgtctg agaacacttt cattttgtaa gccagtgtct 540
69 ccaaggaaag gaatgcagca acaccagcga tgccctggac cctcccctga agaacgtgtc 600
70 cagcaacgca gagtgcctct ctgttatga atctaattga acttcctgtc gtgggaagcc 660
71 ctggaaatgc tatgaagaag aacagtgtgt ctttctagtt gcagaactta agaatgacat 720
72 tgagtctaag agtctcgtgc tgaaaggctg ttccaacgtc agtaacgcc cctgtcagtt 780
73 cctgtctggt gaaaacaaga ctcttgagg agtcacttt cgaaagtttg agtgtgcaa 840
74 tgtaaacagc ttaaccccc cgtctgcacc aaccacttcc cacaacgtgg gctccaaagc 900
75 ttccctctac ctcttgccc ttgccagcct ccttcttcgg ggactgtgc cctgaggtcc 960
76 tggggctgca ctttgcccag caccctattt ctgcttctct gaggtccaga gcacccctg 1020
77 cgggtctgac accctctttc cctgctctgc cccgtttaac tgcccagtaa gtgggagtca 1080
78 caggtctcca ggcaatgccg acagctgcc 1109

```

80 &lt;210&gt; SEQ ID NO: 3

81 &lt;211&gt; LENGTH: 1141

82 &lt;212&gt; TYPE: DNA

83 &lt;213&gt; ORGANISM: Homo sapiens

85 &lt;400&gt; SEQUENCE: 3

```

86 cagagaaaga ggaacatag aggtgccaaa ggaacaaaga cataatgatg tcatccaagc 60
87 caacaagcca tgctgaagta aatgaaacca taccacacc ttaccacca agcagcttta 120
88 tggctccttg atttcaacag cctctgggtt caatcaactt agaaaacaa gctcagggtg 180
89 ctacagcgtg tcagccctat ggcacatcat ctccgggaat ctttgctagc agtcaaccgg 240
90 gtcaaggaaa tatacaaatg ataaatccaa gtgtgggaac agcagtaatg aactttaaag 300
91 aagaagcaaa ggcactaggg gtgatccaga tcatggttg attgatgcac attggttttg 360
92 gaattgtttt gtgtttaata tccttctctt ttagagaagt attaggtttt gcctctactg 420
93 ctgttatttg tggataccca ttctggggtg gcctttcttt tattatctct ggctctctct 480
94 ctgtgtcagc atccaaggag ctttcccgtt gtctggtgaa aggcagcctg ggaatgaaca 540
95 ttgttagttc tatcttgccc ttcataggag tgattctgct gctggtggat atgtgcatca 600
96 atggggtagc tggccaagac tactgggccg tgctttctgg aaaaggcatt tcagccacgc 660
97 tgatgatctt ctccctcttg gagttcttcg tagcttgtgc cacagcccat ttgccaacc 720
98 aagcaaacac cacaaccaat atgtctgtcc tggttattcc aaatatgtat gaaagcaacc 780
99 ctgtgacacc agcgtcttct tcagctcctc ccagatgcaa caactactca gctaattgcc 840
100 ctaaatagta aaagaaaaag gggatatcagt ctaatctcat ggagaaaaac tacttgcaaa 900
101 aacttcttaa gaagatgtct tttattgtct acaatgattt ctagtcttta aaaactgtgt 960
102 ttgagatttg tttttaggtt ggtcgcta at gatggctgta tctcccttca ctgtctcttc 1020
103 ctacattacc actactacat gctggcaaag gtgaaggatc agaggactga aaaaatgatc 1080
104 tgcaactctc ttaaagttag aaatgtttct gttcatatta ctttttctt aataaaatgt 1140
105 c 1141

```

## VERIFICATION SUMMARY

DATE: 07/05/2001

PATENT APPLICATION: US/09/762,021

TIME: 15:50:33

Input Set : A:\Dex-0039.app

Output Set: N:\CRF3\07032001\I762021.raw

L:2 M:283 W: Missing Blank Line separator, <130> field identifier  
L:0 M:201 W: Mandatory field data missing, APPLICANT NAME  
L:0 M:201 W: Mandatory field data missing, TITLE INVENTION  
L:4 M:270 C: Current Application Number differs, Replaced Application Number  
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:52 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

## STATISTICS SUMMARY

PATENT APPLICATION: US/09/762,021

DATE: 07/05/2001

TIME: 15:50:33

Input Set : A:\Dex-0039.app

Output Set: N:\CRF3\07032001\I762021.raw

Application Serial Number: US/09/762,021

Alpha or Numeric: Numeric

Application Class:

Application File Date: 06-11-2001

Art Unit: PCT

Software Application: PatentIn 2.0

Total Number of Sequences: 3

Total Nucleotides: 3960

Total Amino Acids: 0

Number of Errors: 0

Number of Warnings: 5

Number of Corrections: 2

## MESSAGE SUMMARY

201 W: 2 (Mandatory field data missing)

258 W: 1 (Mandatory Feature missing)

270 C: 1 (Current Application Number differs)

271 C: 1 (Current Filing Date differs)

283 W: 1 (Missing Blank Line separator)

341 W: 1 ((46) "n" or "Xaa" used)